

FIG.1

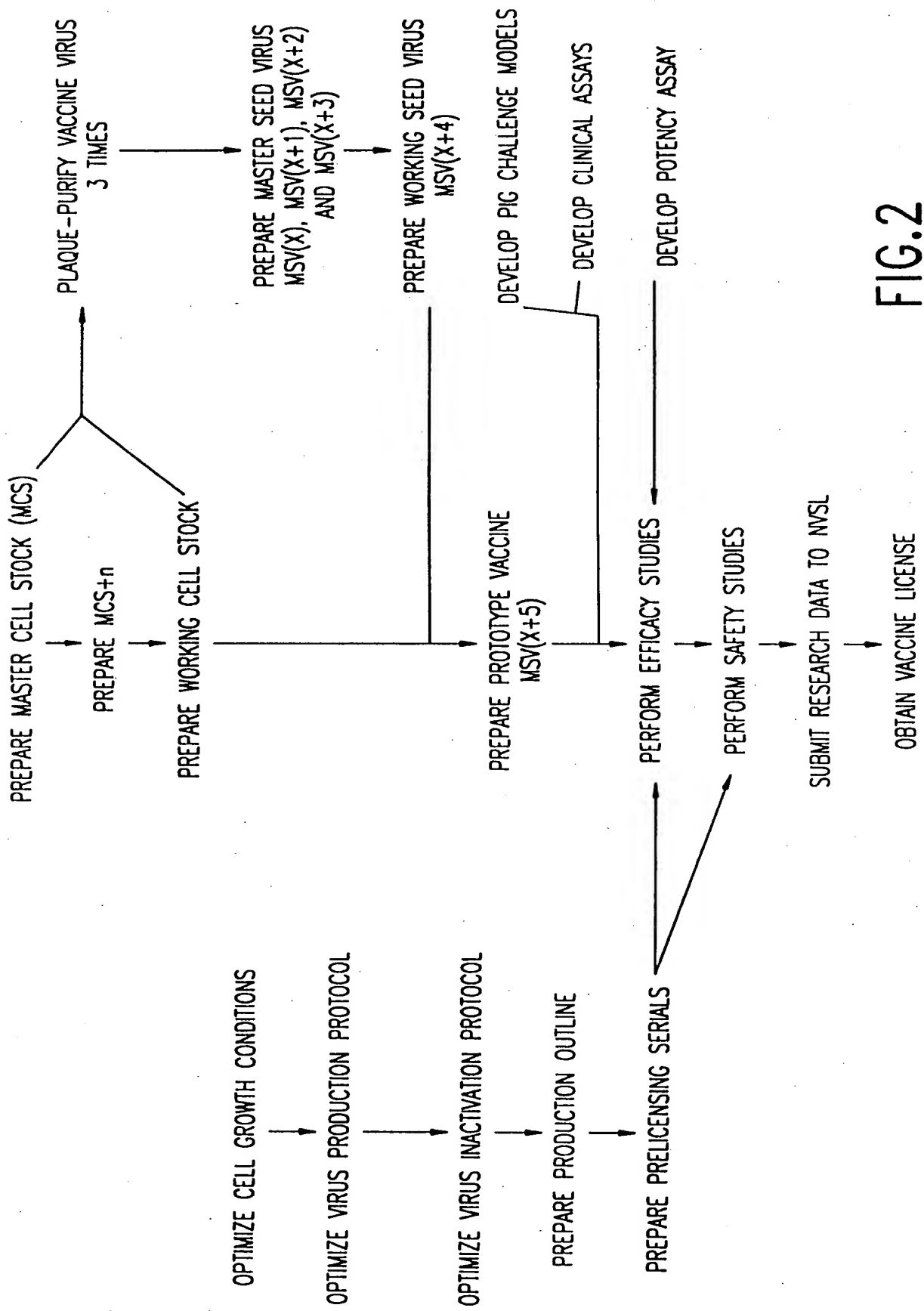
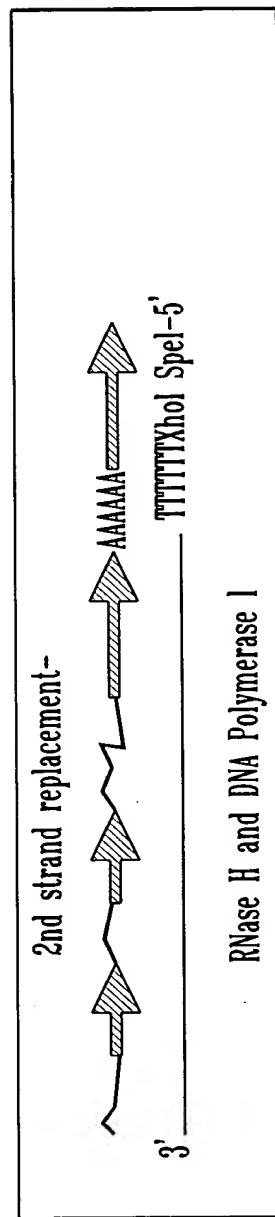
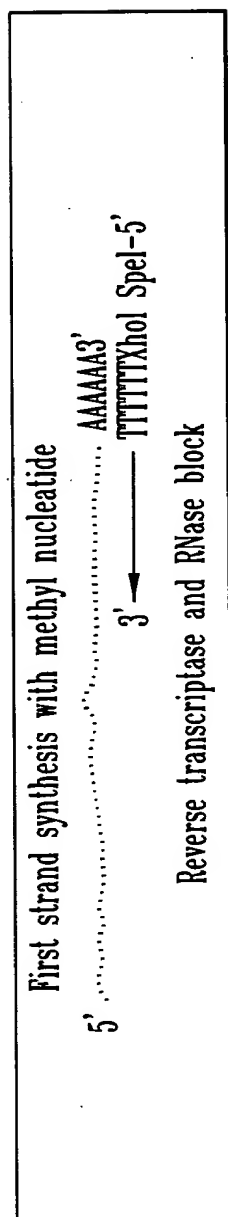


FIG. 2



↓
To Fig.3b

FIG. 3A

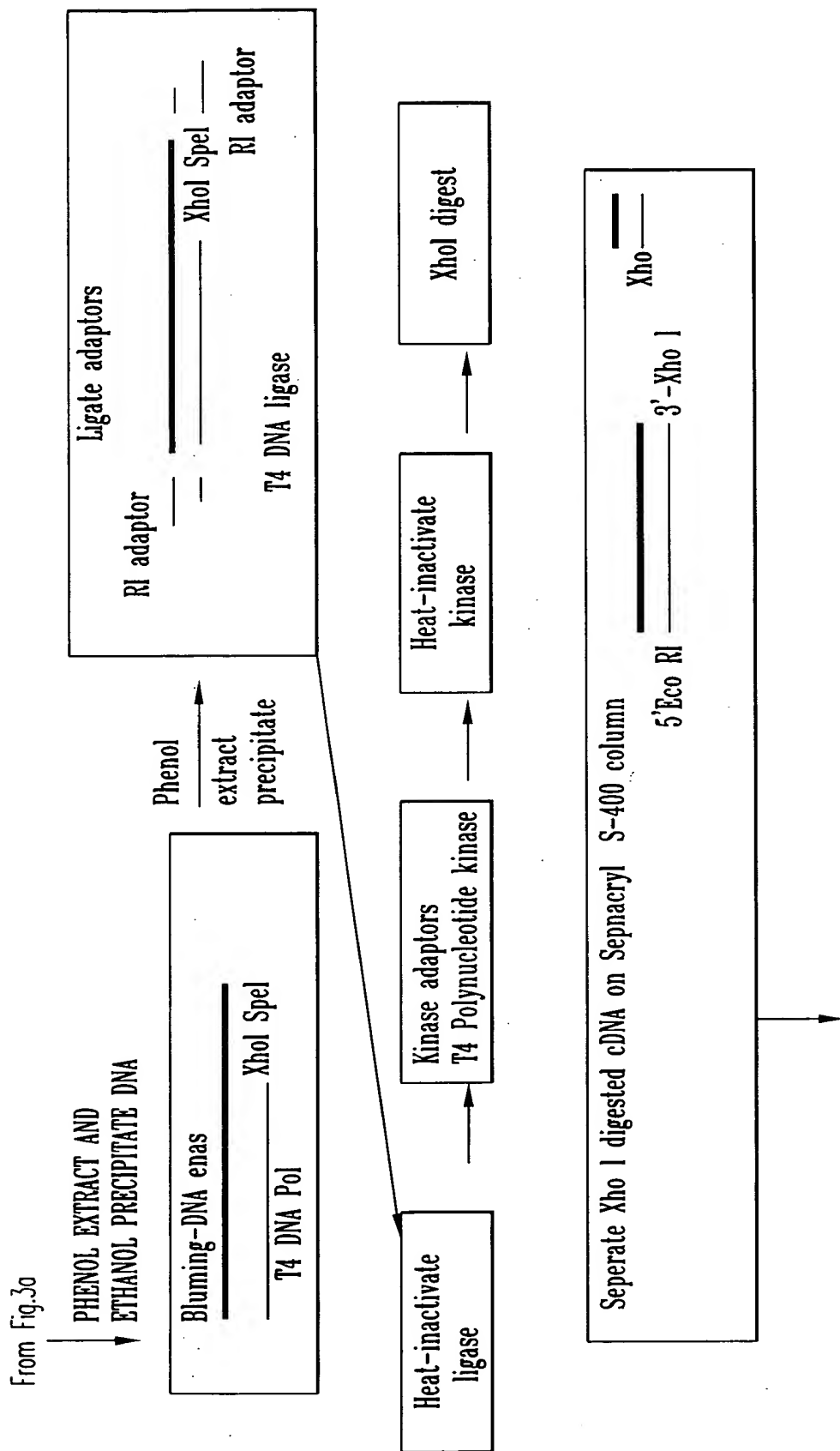


FIG. 3B

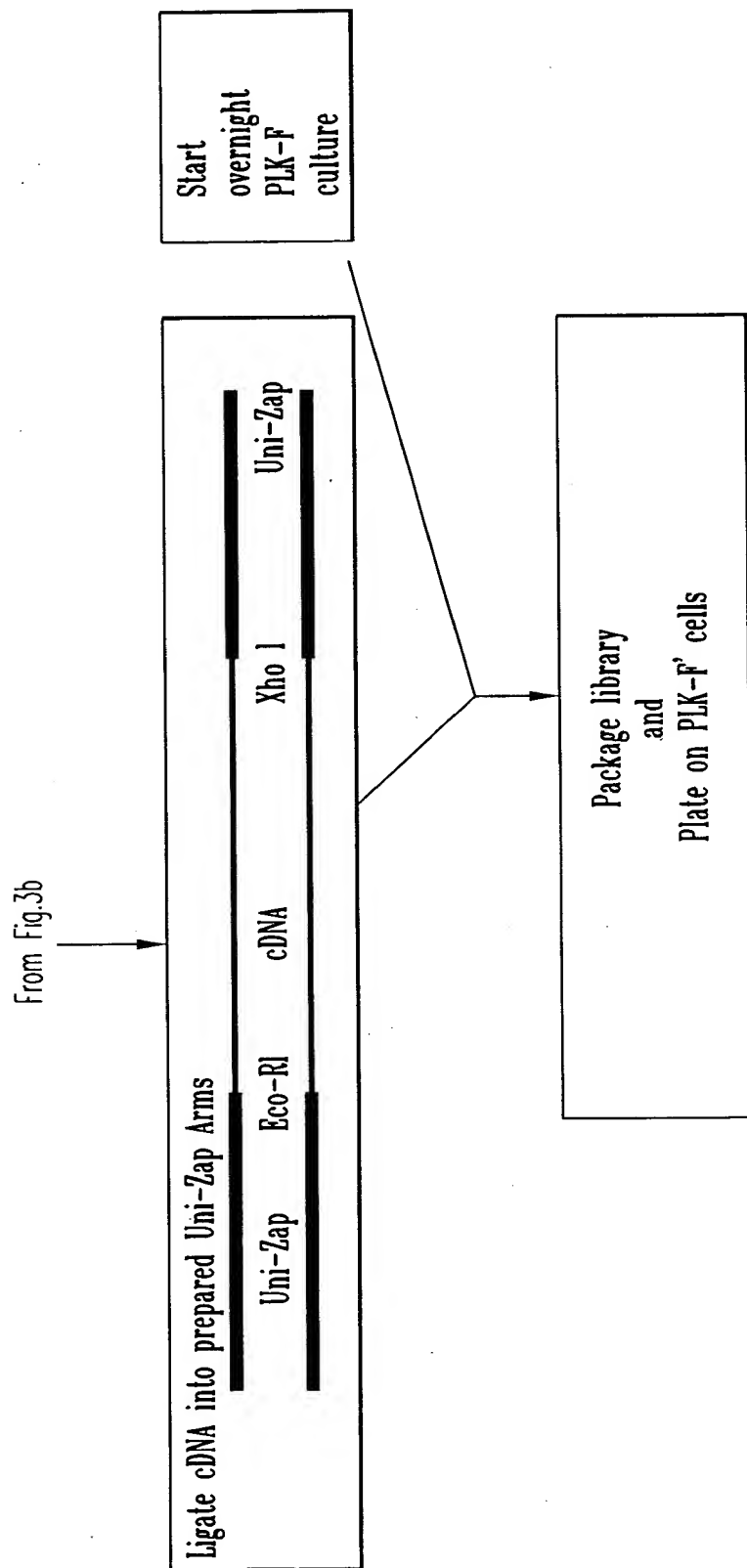


FIG. 3c

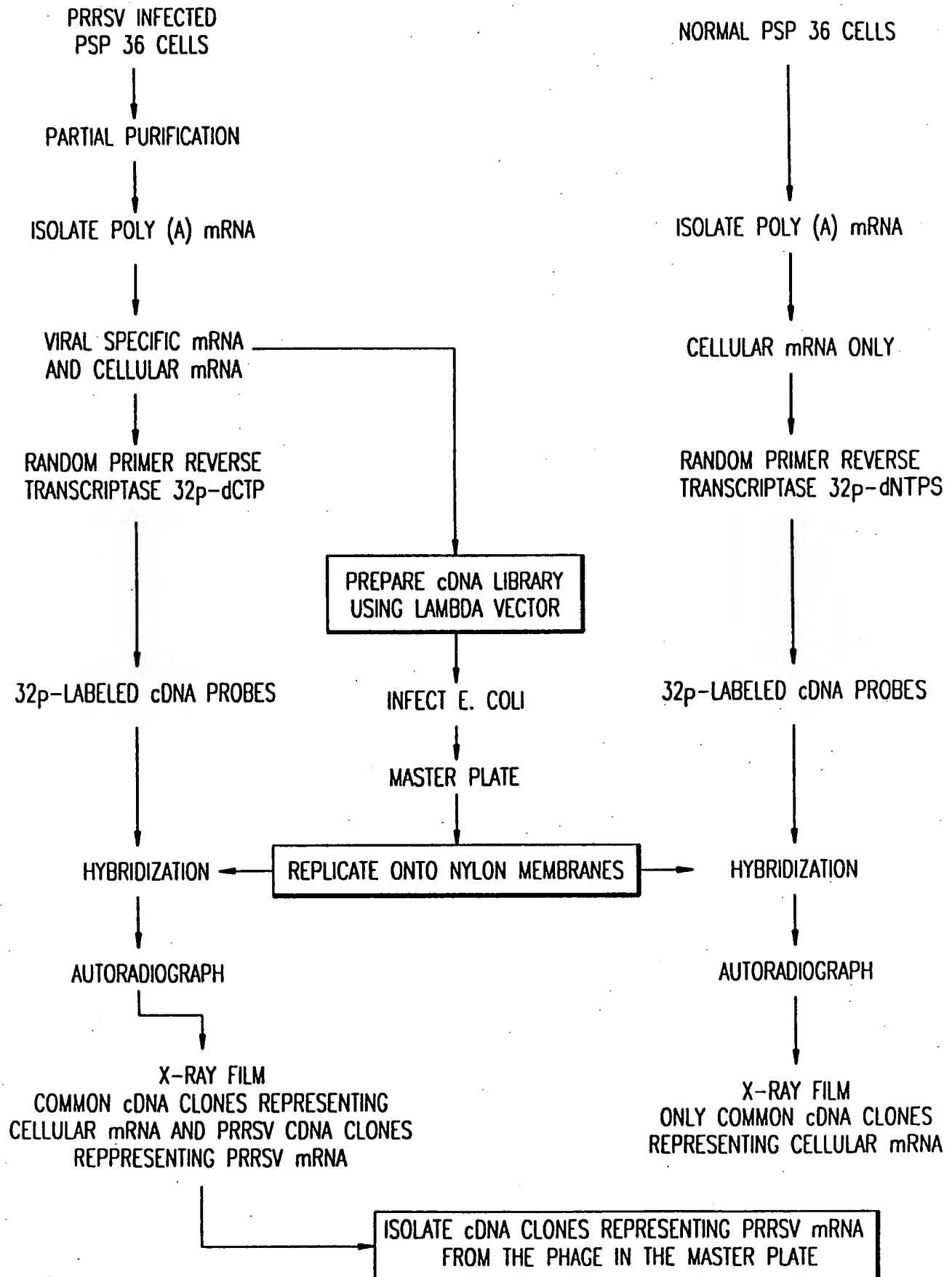


FIG.4

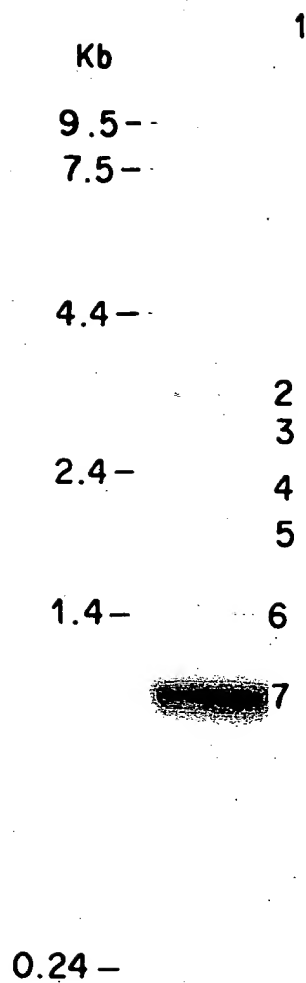


FIG.5

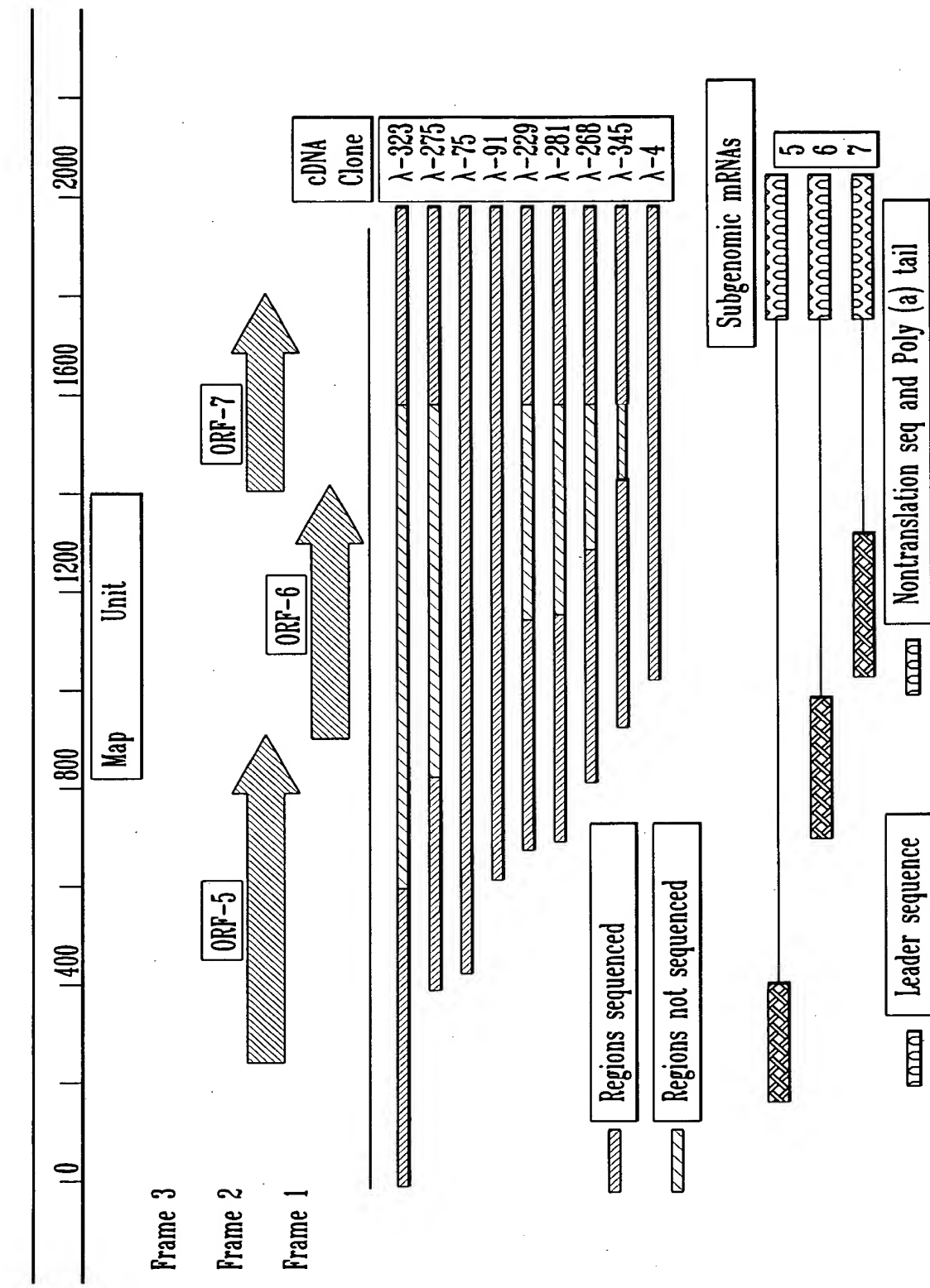


FIG. 6


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GGCAGGCTTTGCTGCTCCTCCAAAGACATCAGTTGCCCTTAGGCATCGCAACTGGCCTCTAGGGCGATTCCGAAAGTCCCTCAGTGCCGCACGGCGATAGGG 100
ACACCCGTGTATACACTGTCACAGCCCAATGTTACCGATGAGAAATTATTGCATTCCCTCIGATCTTCATGCTTTCTCTTGCCCTTTCTATGCTCTG 200
AGATGAGTGAAAAGGGATTAAAGGTGGTATTTGGCAA TGTCAGGGATCGTGCGAGTGTGCGTCAACTTCACCAGTTACGTCCAACATGTC AAGGAATT 300
TACCAACGTTCC TTGGTAGTTGACCATGTGCGGCTGCTCCATTTCATGACGCCCGAGACCATGAGGTGGGCAACTGTTTTAGCCTGTC TTTTTTGGCATT 400
***
DRF4 stop
***
+1>DRF5 start
CTGTTGGCAATTGAATGTTAAGTATGTTGGGAAATGCTTGACCGCGGGCTGTGTGCTCGCAATTGCTTTTTTGGTGATCGTGCCGCTCTGTTTT 500
GTTGCGCTCGTCAGCGCCAACGGGAACAGCGGCTCAAATTTACAGCTGATTTACAAC TTGACGCTA GTGAGCTGAATGGCACAGATTGGCTAGCTAATA 600
AATTTGACTGGGCAGTGGAGTGTTTTGTCATTTTCCTGTTGACTCAGATTGTCCTTATGGTGCCCTCAGTACTAGCCATTTCC TTGACACAGTCGG 700
TCTGGTCACTGTGCTACCGCTGGGTTGTTACGGGGGGTATGTTCTGAGTAGCATGTACGGGCTCTGTGCCCTGGCTGGCTGATTGCTTCGTCATT 800
AGGCTTCCGAAGAA TTGCATGTCCTGGCGCTACTCATGTACCAGATATACCAACTTCTCTCGACACTAAGGGCAGACTCTATCGTTGGCGGTGCGCCTG 900
TCATCATAGAGAAAAGGGGCAAAGTTGAGGTGGAAGGTCACCTGATCGACCTCAAAAGAGTTGTGCTTGATGGTTCGCGGGCTACCCCTGTACCAGAGT 1000
DRF6 start
+1>
***DRF5 stop
TTCACGGGAACAAATGGAGTCGTCCTTAGATGACTTCTGTCATGATAGCAGGCTCCACAAAGGTGCTCTTGGCGTTTTCTATTACCTACACGCCAGTGA 1100

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FIG. 7A

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TGATATATGCCCTAAAGGTGAGTCGGCGGCGACTGCTAGGGCTTCGTGACCCTTTGGCTCTCCTGAAATTGTGCTTTCACCTTCGGGTACATGACATTCGT 1200

GCAC TTCAGAGTACAAATAAGGTGCGGCTCACTATGGGAGCAGTAGTTGCACTCCTTTGGGGGGGTGACTCAGCCATAGAAACCTGGAAATTCATCACC 1300

TCCAGATGCCGCTTGTGCTTGTAGCGCGCAAGTACATTCTGGCCCTGCCACCACGTTGAAAGTGGCGGAGGCTTTCATCCGATTGGCGCAAATGATA 1400

ACCACGCATTTGTCTCGGGTCCCGGCTCCACTACGGTCAACGGCACATTGGTGCCCGGGTTAAAAAGCCTCGTGTGGGTGGCAGAAAAGCTGTTAA 1500
      DRF7 start
      +1> ***DRF6 stop
ACAGGGAGTGGTAAACCTTGTAAATATGCCAAATAACACCGGCAAGCAGCAGAGAGAGAAAGGGGGATGGCCAGCCAGTCAATCAGCTGTGCCAGAT 1600

GCTGGGTAAAGTATCGCTCACCAAAACCAGTCCAGAGGGCAAGGACCGGGAAAGAAAAATAAGAGAAAAAACCCGGAGAGCCCCATTTCCTCTAGCG 1700

ACTGAAGATGATGTCAGACATCATTACCCCTAGTGAGGCTCAATTGTGCTGTCTCAATCCAGACCGCCTTAAATCAAGGGCTGGGACTTGCACCC 1800
      ***DRF7 stop
TGTCAGATTCAGGGAGGATAAGTTACACTGTGGAGTTTAGTTTGCTTACGCATCATACTGTGGCCTGATCCGGGTACAGCATCACCCCTCAGCATGATG 1900

GGCTGGCATTCCTTGAGGCATCCAGTGTGTGAATTGGAAGATGGGTGGTGAATGGCACIGATTGACATTGTGCCTCTAAGTCACCTATTCAATTAGGGC 2000

GACCGTGTGGGGGTAAGATTTAATTGGCGAGAACACACGCGCGAAATTAAAAAAAAAAAAA 2062

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FIG. 7B

LELYSTAD SEQ (13484-14089)	ATGAGATGTTCTCACAAATGGGGCGTTTCTTGACTCCGCACCTCTTGGCTTCTGGTGGCTTTTTTTCGCTGIGTA--	13556
ISU-12-3' TERMINAL (426-1028)	-----ATGTGGGGAAATGCTTGACCCGGCTCTTGGCTGGCAATTTGCTTTTTTGTGGGTATC	485
LELYSTAD SEQ (13484-14089)	---CCGCTTGTCTCTGGT-CCTTTGGGATGGCAACGGCCACAGCTCGACATACCATAA-C-ATAATATAACTTG	13624
ISU-12-3' TERMINAL (426-1028)	GTCCGTCCTTGTTTGTGGGCTCTGAGCCCAACGGGACAGGGCTCAAAATTACAGCTGATTTACAACTTG	560
LELYSTAD SEQ (13484-14089)	ACGATATGGAGCTGAATGGACCGACTGGTTGTCCAGCCATTTTGGTTGGGCAGTGGAGACCTTTGTGCTTTAC	13699
ISU-12-3' TERMINAL (426-1028)	ACGCTATGTGAGCTGAATGGACAGATTGGCTAGCTAATAAATTTGACTGGGCAGTGGAGTGTTTTGTCATTTTT	635
LELYSTAD SEQ (13484-14089)	CCGGTTGCCACTCATAATCCCTCTCACTGGGTTTCTCACAAACAGCCATTTTGTGACGGCTCGGTCCTCGGCTCT	13774
ISU-12-3' TERMINAL (426-1028)	CCGTGTTGACTCACAATGTCCTCTTATGGTGGCTCCCTCACACTACTAGCCATTTCTTGACACAGTGGGTCTGGTCACT	710
LELYSTAD SEQ (13484-14089)	GTAATCACTGCAAGATTGTTGGGGGGCGGTAGGTACTCTGCAGCGTCTACGGGCTTGTGGCTTTGCGAGCGGTTC	13849
ISU-12-3' TERMINAL (426-1028)	GTGCTACCGGCTGGTTTGTTCACGGGCGGTATGTCTGAGTAGCAATGTACCGGTGTGTGGCCGTGGCTGGCTTG	785
LELYSTAD SEQ (13484-14089)	GTATGTTTGTTCATCCGTGCTGCTTAAATAATTGATGGCTCCGGCTATGCCCGTACCGGGTTTACCAACTTCATT	13924
ISU-12-3' TERMINAL (426-1028)	AATTTGCTTGGTCAATAGGCTTGGCAAGCAATTGCAATGCTCCCTGGCTACTCATGTACCAAGATATACCAACTTTCTT	860
LELYSTAD SEQ (13484-14089)	GTGGACGACCGGGGAGAGTTTCAATCGATGGAAATCTCCAAATAGTGGTAGAAATAATGGGCAAAAGCCGAAGTCCGAT	13999
ISU-12-3' TERMINAL (426-1028)	CTGGACACTAAGGGCAGACTCTATCGTTGGCGGTGCGGTGTCATTCATAGACAATAAGGGCAAAAGTTGAGGTCCGAA	935
LELYSTAD SEQ (13484-14089)	GGCAACCTCGTCAACCAATCAAAACATGTGCTCTCGAAGGGGTTAAAGCTCAACCCCTTTGACGAGACTTCGGGTGA	14073
ISU-12-3' TERMINAL (426-1028)	GGTCACCTGATCGACCTCAAAAGAGTTGTGCTTGATGGTTCCGGCGCT-ACCCCTGTAAACCAAGTTTTCAGGGGA	1009
LELYSTAD SEQ (13484-14089)	GCAATGGGAGCCCTAG-----	14089
ISU-12-3' TERMINAL (426-1028)	ACAAATGGAGTCTCTCTTAG	1028

FIG. 8

ISU 12/7a/3' terminal (888 – 1413)	AATGGAGTGG TCGTTAGATG ACTTGTGTCA TGATAGCAGG GGTCCACAAA AGGTGCTCTT	947
LeIystad seq (14077 – 14598)	-ATGG-GAGG --CGTAGAGG ATTITITGCAAT CGATCCATATC GCGGCACAAA AGCTCGTGGT	14132
ISU 12/7a/3' terminal (888 – 1413)	GGCGTTTCT ATTAACCTACA CCGCAGTGAAT GATATATGCC CTAAAGGTGA GTCCCGGCGG	1007
LeIystad seq (14077 – 14598)	AGCGTTTJAGC ATCACAATACA CACCTATTAAT GATATAAGCC CTAAAGGTGT CACCGGCGCG	14192
ISU 12/7a/3' terminal (888 – 1413)	ACTGCTAGGG CTTCGTGACC TTTTGGTCTT CTGAATTTGT GCTTTCACT TCGGATACAT	1067
LeIystad seq (14077 – 14598)	ACTGCTAGGG CTGTTGCCACA TCCCTAATATTT TCTGAACITGT TCGTTTACAT TCGGATACAT	14252
ISU 12/7a/3' terminal (888 – 1413)	GACATTCGTG CACTTTCAGA GTACAATAA GGTCGGGCTC ACTATGGGAG CAGTAGTTGC	1127
LeIystad seq (14077 – 14598)	GACATATGTG CATTTTCAAT CCACCAACCG TGTCGGACIT ACCCTGGCGG CTGTTTCTGG-	14311
ISU 12/7a/3' terminal (888 – 1413)	ACTCCTTTGG GGGGTGTAAT CAGG-CATA GAAACCTGGA AATTCAATCAC CTCCAGATGC	1185
LeIystad seq (14077 – 14598)	-CCCTTTCTGT GGGGTGTTTA CAGCTTCACA GACTCATGGA AGTTTATCAC TTCCAGATGC	14370
ISU 12/7a/3' terminal (888 – 1413)	CGTTTGTGCT TGTAGCCCG CAAGTACAT CTGGCCCCCTG CCCACACAGT TGAAGTGGC	1245
LeIystad seq (14077 – 14598)	AGATTGTGTT GCCTTGCGCG GCCATACAT CTGGCCCCCTG CCCATCACGT AGAAGTGGT	14430
ISU 12/7a/3' terminal (888 – 1413)	GCAGGCTTTC ATCCGATTC GCGAAATGAT AACCAAGCAT TTGTGCTCGG CCGTCCCGGC	1305
LeIystad seq (14077 – 14598)	GCAGGTCTCC ATTCAATCTC AGCTGTGCT AACCGAGCAT ACGCTGTGAG AAAGCCCGGA	14490
ISU 12/7a/3' terminal (888 – 1413)	TCCACTACCG TCAACGCCAC ATTGCTCCC CCGTTAAAAA GCCTCGTGT TGGTGGCAGA	1365
LeIystad seq (14077 – 14598)	CTAACAATAG TGAACGCCAC TGTAGTACCA GGAATTCGGA GCCTCGTGT TGGTGGCANA	14550
ISU 12/7a/3' terminal (888 – 1413)	AAAGCTGTTA AACAGCGAGT GGTTAAACCTT GTTAATATATG CCAAAATAA	1413
LeIystad seq (14077 – 14598)	CGAGCTGTTA AACAGCGAGT GGTTAAACCTC GTTAAGTATG GCGGTAA	14598

FIG. 9

Lelystad seq (14588 – 14974) ISU 12/7a/3' terminal (1403 – 1774)	ATGGCCGGTA AAACCAAGAT- -----AT GCCAAGAGAA GCCAATATAC ACCGCAAGC AGCAGAAGAG	14632 1434
Lelystad seq (14588 – 14974) ISU 12/7a/3' terminal (1403 – 1774)	TCCGATGGGG AATGGCCAGC CAGTCAATCA AAACAAGGGG GATGGCCAGC CAGTCAATCA	14681 1483
Lelystad seq (14588 – 14974) ISU 12/7a/3' terminal (1403 – 1774)	CAATGATAAA GTCCACGGC CACCAACCTA -AA-CATCAT CCCTCAGAA AACCAGTCCA GAGCAAGGG ACCGG--GA	14728 1528
Lelystad seq (14588 – 14974) ISU 12/7a/3' terminal (1403 – 1774)	AAGAAAAA ----- -CCTGAGAAG CCTCATTTTC CCTTCCTGC AAGAAAAA AGAAAAATA AGAAAGAAAA CCCGGAGAAG CCTCATTTCC CTCTAGCGAC	14766 1578
Lelystad seq (14588 – 14974) ISU 12/7a/3' terminal (1403 – 1774)	TGAAGATGAC ATCCCGCACC AOCCTACCCA GACTGAAAGC TCCCTTCCT TGAAGATGAT GTCAAGATAC ACTTTACCCC TAGTGACCGT CAATTGTGTC	14816 1628
Lelystad seq (14588 – 14974) ISU 12/7a/3' terminal (1403 – 1774)	TGCAATCGAT CCAGACGGGT TGTCGTGAT CCAGACCGCC TTTAAATCAAG GCGCTGGCAG -TTCGCTCCCT TTGCAAG-C	14865 1677
Lelystad seq (14588 – 14974) ISU 12/7a/3' terminal (1403 – 1774)	TTTCATCCAGC GGGAGGTCA GTTTTCAGGT TGAGTTTATG GTCCCGTTTG GTCAGATTCA GGGAGCATAA GTTACACTGT GGAGTTTACT TTCCCTACGC	14915 1727
Lelystad seq (14588 – 14974) ISU 12/7a/3' terminal (1403 – 1774)	CTCATACAGT CGGCTGATTT CGCGTCACTT CTACATCCGC CAGTCAAGGT ATCATACTGT CGGCTGATC CGCGTCAAG CATCACCC-T CAG-CATGA-	14965 1774
Lelystad seq (14588 – 14974) ISU 12/7a/3' terminal (1403 – 1774)	GCAAGTTAA	14974 1774

FIG.10

ISU 12/7a/3' terminal (1775 - 1938)	1814
Lelystad seq (14975 - 15101)	14976
	<p> TGGCTGGCA TTCTGAGGC ATCCAGTGT TTGAATGGA -----TT </p>
ISU 12/7a/3' terminal (1775 - 1938)	1854
Lelystad seq (14975 - 15101)	15016
	<p> AGAAATGGTG GTGAATGGCA CTGATTGACA TTGTCCTCT TGACAGTCAG GTGAATGGCC GCGATTGGCG TTGTCCTCT </p>
ISU 12/7a/3' terminal (1775 - 1938)	1800
Lelystad seq (14975 - 15101)	15056
	<p> AGTCACCTA TTCAATTAGG GCGACCGTGT GGGGGTAACA GAGTCACCTA TTCAATTAGG GCGATCACAT GGGGGTCAATA </p>
ISU 12/7a/3' terminal (1775 - 1938)	1933
Lelystad seq (14975 - 15101)	15096
	<p> TTTAATT-GG CGACAACCAC ACACCGGAAA TTAAAAAAA CTTAATCAGG CAGCAACCAT GTACCGGAAA TTAAAAAAA </p>
ISU 12/7a/3' terminal (1775 - 1938)	1938
Lelystad seq (14975 - 15101)	15101
	<p> AAAAA AAAAA </p>

FIG. 11

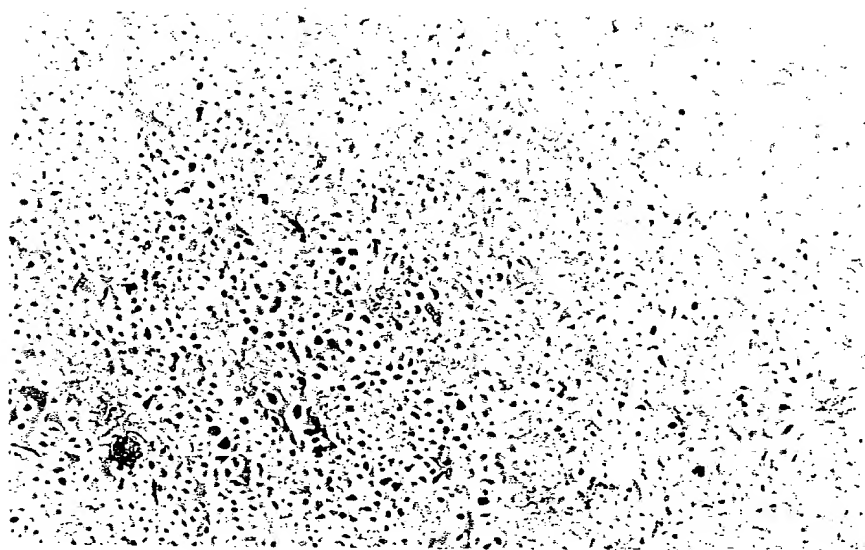


FIG.12

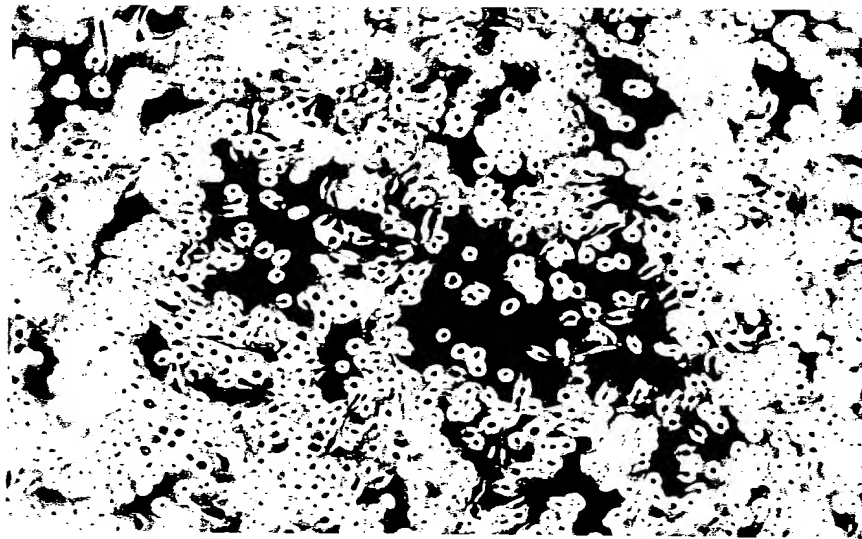


FIG.13

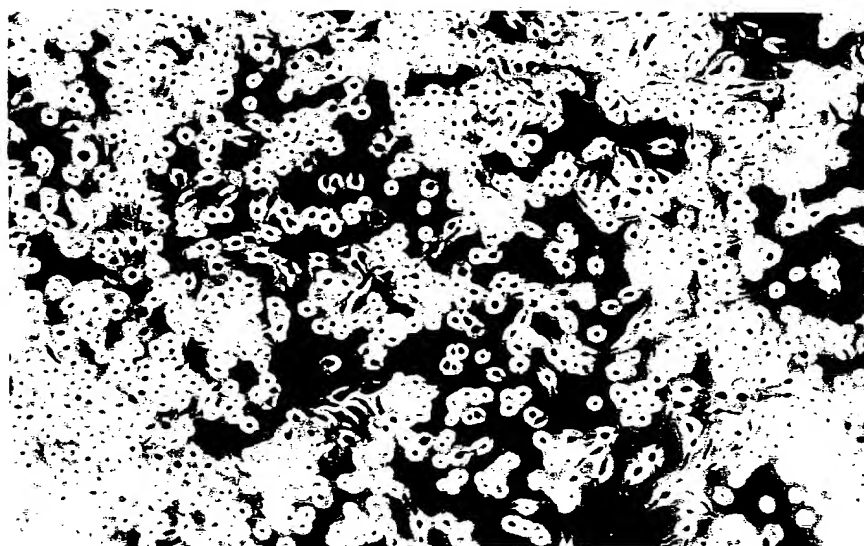


FIG.14

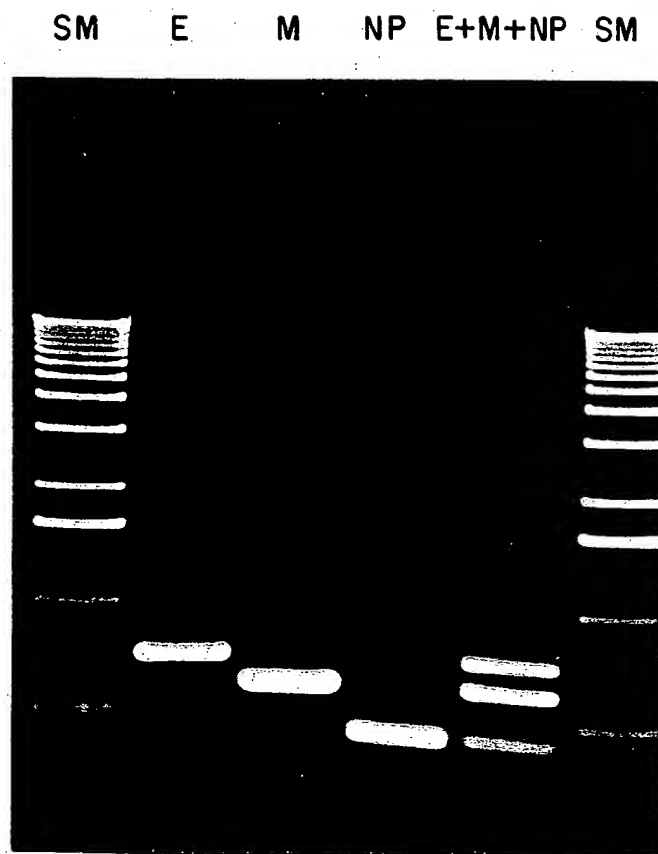


FIG.15

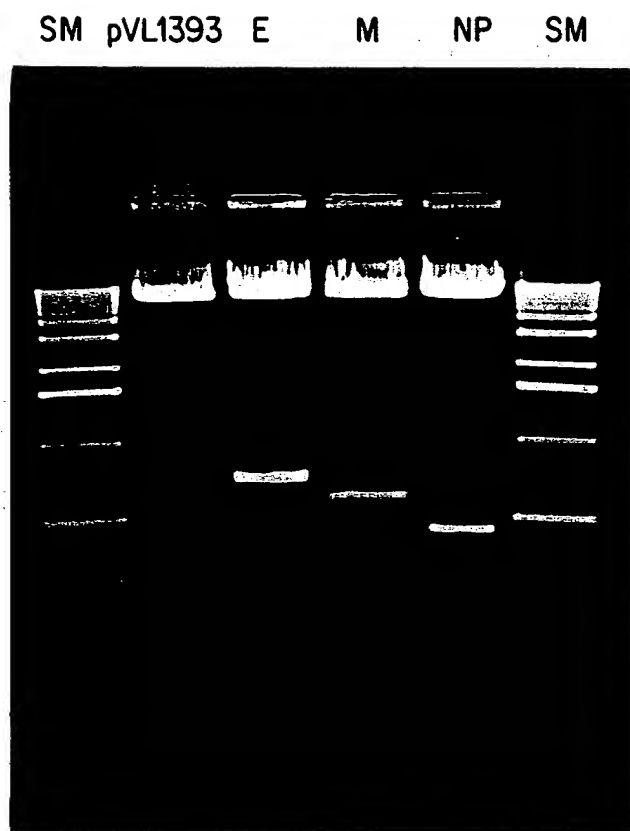


FIG.16

Accession	Sequence	Length
VR 2385	ATGGAGTCGCTCCTTAGATGACTTCCTGTCATGATAGCACGGCTCCACAAAAGGTGCTCTTGGCGTTTCTATTACCTACACGCCAGTGATGATATATGCCC	100
ISU-1894G.....C.....T.....T.....	100
ISU-22G.....C.....T.....	100
ISU-79G.....T.....T.....A.....	100
ISU-55G.....C.....T.....C.....	100
ISU-3927G.....C.....T..CA.....T.....G.....T.....	100
LVG--A--G.C....C..T..T..CA.C....CCT.TC..CG.....C.CG.GC.A.C....AGC..C..A....TA.A.....C....	97

VR 2385	TAAAGGTGAGTCCGCGCCGACTGCTAGGGCTTCGACCTTTTGGTCTTCCTGAAATTGTGCTTTTCACCTTCGGGTACATGACATTCGTCGACTTTCAGAG	200
ISU-1894A.....	200
ISU-22	G.....A.....	200
ISU-79A.T.....C.....A.....	200
ISU-55	...A.A.....A.....A.....	200
ISU-3927A.....A.T.T.....T.T.....G.....	200
LV	.T.....TCA.....C.G.....GT.....A.CC.AA.A.T.....C...T.C...T..A.....A.....AT.....T.....ATC	197

VR	2385	TACAAATAAGGTCCGCTCACTATGGGAGCAGTAGTTGCACCTCCCTTTGGGGGGGTGTACTCAGC--CATAGAAACCTGGAAATTCATCACCCTCCAGATGCC	298
ISU-1894		298
ISU-22	A.....	298
ISU-79	298
ISU-55	C.....C.....	298
ISU-3927	C.....G.....C.....T.C.....	298
LV	C..C..CCGT.....A..T..CC.....G..T..T..C..C..--CCT..C..T.....TIA.....TT..C...GT..A.....G..T....T.....A	295

FIG. 17A

VR 2385 GTTGTGCTAGGCGCAAGTACATTCTGGCCCCTGCCACCACGTTGAAAGTGCCGCAGGCTTTCATCCGATTGCGGCAAAATGATAACCACGCATT 398
 ISU-1894 398
 ISU-22 398
 ISU-79 398
 ISU-55 A 398
 ISU-3927 G 398
 LV A TGC T TC C T A CT A GTC G GA A 395

VR 2385 TGTGTCGGGGTCCCGCTCCACTACGGTCAACGGGCACATTGGTGCCCGGGTTAAAAAGCCTCGTGTGGGTGGCAGAAAAGCTGTTAAACAGGGAGTG 498
 ISU-1894 G 498
 ISU-22 T G 498
 ISU-79 G 498
 ISU-55 T G C 498
 ISU-3927 T G G A G 498
 LV C, CT, GA, AAAG, ACTA, AT, A, G, TC, A, A, A, AC, TCGG, C, C, A, CG, GA, 495

DRF 7 start

+ 1> *** DRF 6 stop

VR 2385 GTAAACCTTGTTAAATATGCCAAATAACACCGGCA-AGCAGCAGAGAGAAAGAA-----GGGGGATGGCCAGCCAGTCAATCAGCTGTG 582
 ISU-1894 C A 582
 ISU-22 C A T 582
 ISU-79 C A 582
 ISU-55 582
 ISU-3927 A A 582
 LV T C C G G CGG A A G AAGTACAGCTCCGAT A A 591
 AAAAAAAAAAAAAAAAAA

FIG. 17B

VR 2385	CTTGACC-CTGTCAGATT	CAGGAGGATAAGTTACAC	TGTGGAGTTAGTTGGCTACGCATCATACTGTGGCCTGATCCGGT	CACAGCATCACCC-	877
ISU-1894A.....T.....	877
ISU-22	877
ISU-79T.....	877
ISU-55T.....G.....G.....	877
ISU-3927	C..T.T..A..G.....T.....G..C.....	877
LV	...GT.G..T...TCCAGC...	A.G.C...TTCAG..T...TGC...	GGTTGC.....A.....T.....G..TT..TA..T..G		878

VR 23 85	TCAG-CA-----TGA	886
ISU-1894	886
ISU-22	886
ISU-79	886
ISU-55	886
ISU-3927	886
LV	C...T..GGGTGCAAGT..A. ^^^^^^^^^^	898

FIG. 17D

VR 2385 DRF6	MESSLDDFCHDSTAPQKVLLAFSITTPVMIYALKVSRGRLLGLLLVFLNCAFTFGYMTFVHFQSTNKVALTMGAVVALLWGVYSAIETWKFITSRCR	100
ISU-1894 DRF6	.G.....I.....	100
ISU-22 DRF6	.G.....I.....	100
SIU-55 DRF6	.G.....I.....	100
ISU-79 DRF6	.G.....Y.....M.....	100
ISU-3927 DRF6	.G.....N.....I.....E..R.....	100
LV DRF6	.G-G.....N.PI.A..LV.....I.....S.....Y.....R...L.....FT.S.....	99
PRRSV-10 DRF6	.G-G.....N.PI.A..LV.....I.....S.....Y.....R...L.....FT.S.....	99
LDV-C DRF2	.G-G..-E..DQTSWY..-IFI..L....IA..S...F..T..A..IVNIFI..I...CVS..V..LMYH..-SV..TI..SL...I..V..I..TLVKIVDVLVI...	96
LDV-P DRF2	.G-G..-E..DQTSWY..-I..I...L....IA..S...F..T..A..IVNIFI..I...CVS..V..LMYH..-SV..T...SL...I..V..I..TLVKIVNMMVL...	96

VR 2385 DRF6	LCLLGRKYILAPAHHVESAAAGFHPAANDNH-----AFVVRPRPGSTTVNGTLVPGLKSLVLGGRKAVKQGVVNLVKY-AK	183
ISU-1894 DRF6-----.....	174
ISU-22 DRF6-----.....	174
SIU-55 DRF6-----.....	174
ISU-79 DRF6-----.....	174
ISU-3927 DRF6-----R.....K.....	174
LV DRF6	..C...R.....L.S.S.SG.R-----YA..K..L.S.....R.....KR...R.....-GR	173
PRRSV-10 DRF6	..C...R.....L.S.S.SG.R-----YA..K..L.S.....R.....KR...R.....-GR	173
LDV-C DRF2	..F...S....PS.,D-----TSDGRQSLTTSITT....K...L...Q...DFQR.....K...SK.A...L...VS,	171
LDV-P DRF2	..F...S....PS.,D-----TSDGRQSLTTSITT....K...L...Q...DFQR.....K...SK.A...L...VS,	171

FIG. 18A

VR 2385 DRF7	MPNNTGKQQRKK-----GDGQPVNQLCQMLGKIIAHQNSRGKGPCKKNKKKNPEKPHFPLATEDDDVRHHFTPSERQLCLSSIQTAFNQGAGTCTLS	100
ISU-1894 DRF7N.....-----Q.....	93
ISU-22 DRF7N.....-----Q.....	93
ISU-79 DRF7N.....-----Q.....	93
ISU-3927 DRF7N.....K.....-----Q.....	93
ISU-55 DRF7N.....K.....-----Q.....SG.....	93
VR2332 DRF7N.....TEE.....-----Q.....	93
LV DRF7-A...N.SQ.,KKSTAPM,N.....L.,AM.KS.R.,---QPR,GQA...K.....A...I...L,QT...S...Q.....AS...	94
PRRSV-10 DRF7-A...N.SQ.,KKSTAPM,N.....L.,AM.KS.R.,---QPR,GQA...K.....A...I...L,QT...S...Q.....PS...	94
LDV-C DRF1	..SQ,KK.GGQN.....AN,---,N.LISALLRNAG,--N.,K.Q.K.,-Q-,L...M.GPS,L.,VM.,N.V.M.R.,LV,L.,...G.Q.,...V	85
LDV-P DRF1	..SQ,KK.SGQN.....AN,---,N.LINALLRNAG,--N.,K.Q.K.,-Q-,L...M.GPS,L.,VM.,N.V.M.R.,LV,L.,...G.Q.,...V	85
EAV DRF7	..ASRRSRP,AASF-----RN,R--RRQPTSNDLLRMFG,-----MRVR,PPAQPTQATI,EPG,L.,DLNQQ.,ATLS,NV,RF,MI,H.SL,-A	83

^^^^^^

VR 2385 DRF7	DJSGRISYTFEFSLPTHHTVRLIRVTASP-----SA	134
ISU-1894 DRF7	123
ISU-22 DRF7	123
ISU-79 DRF7	123
ISU-3927 DRF7P,-----	123
ISU-55 DRF7	123
VR2332 DRF7	123
LV DRF7	..S.,KV,FQ...M.,VA.....,STSASQGAS	128
PRRSV-10 DRF7	..S.,KV,FQ...M.,VA.....,STSASQGAS	128
LDV-C DRF1G,NF...S.M.,...A.....,NAS,NS-----	115
LDV-P DRF1G,NF...S.M.,...A.....,NAS,NS-----	115
EAV DRF7	..A,GLT,...SW-V.,KQIQ,KVAPP,G,-----	110

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FIG. 18B

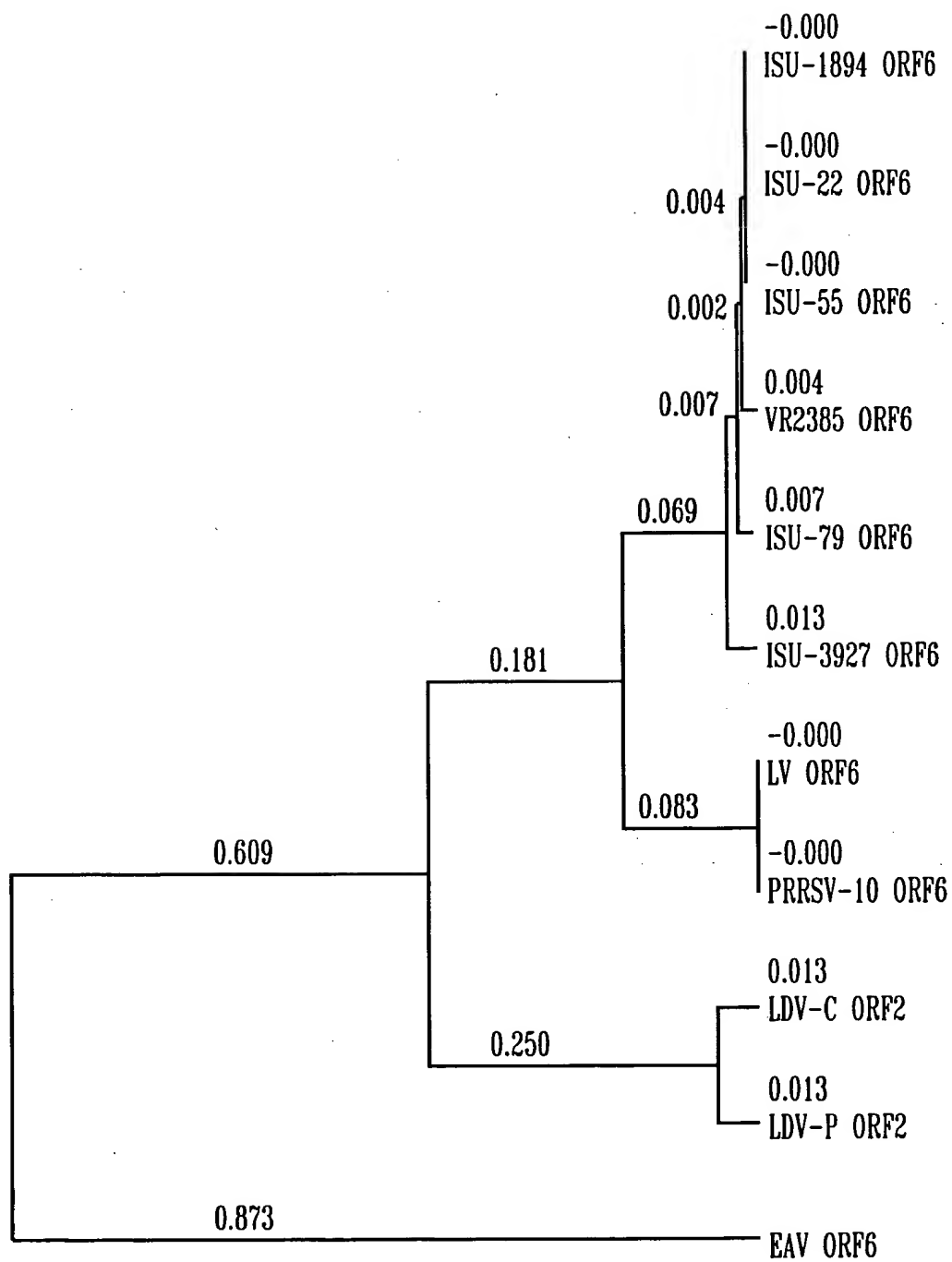


FIG. 19A

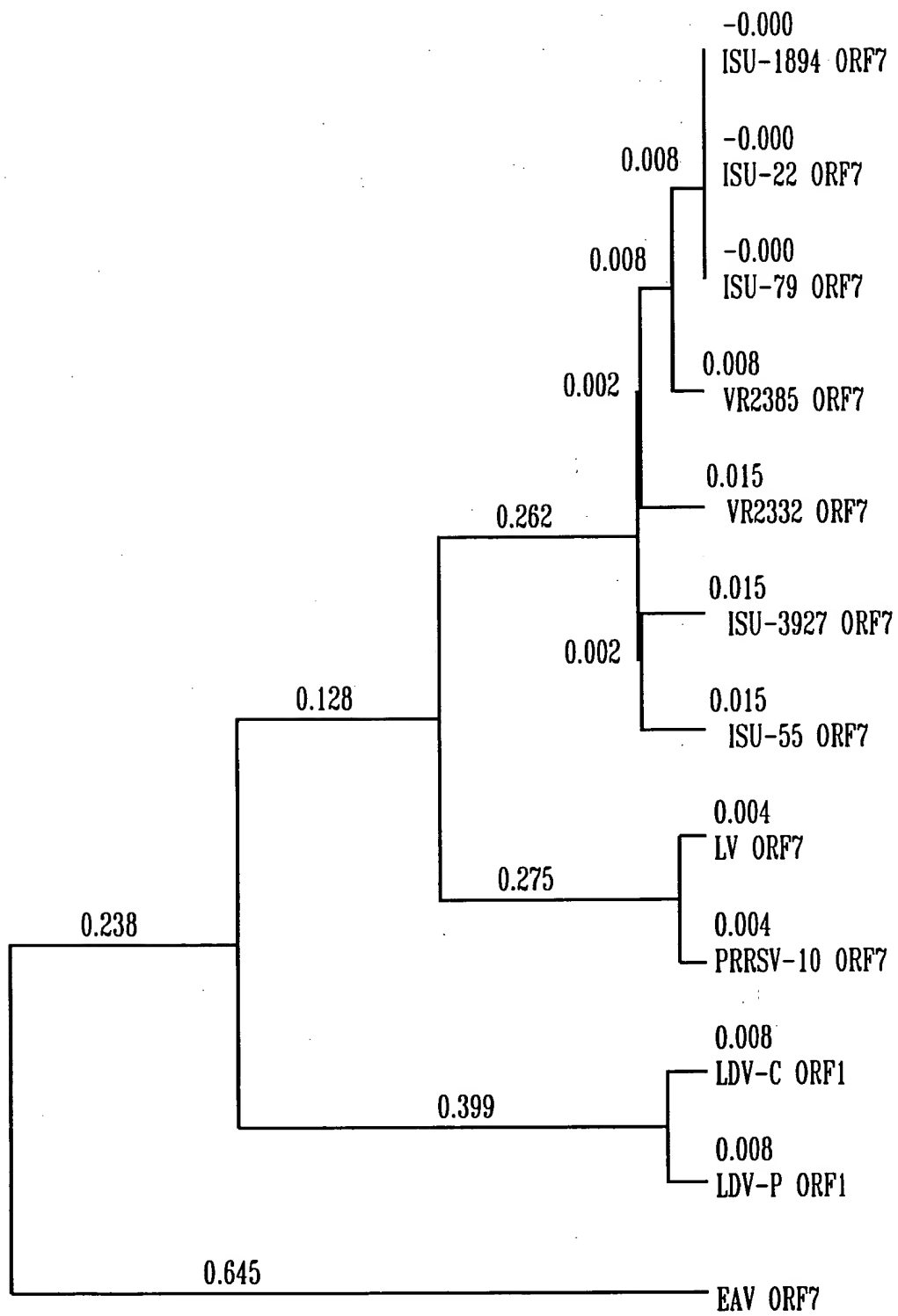


FIG. 19B

+ Start DRF2

100 CCTGAATTGAGATGAAATGGGGTCTATGCAAAAGCCTTTTGGCCAACTTTTGTGGATGCTTTCACGGAGTCTTGGTGCCATTGTTGAT

200 ATCATTATATTTTGGCCATTTTGTGGCTTACCATCGCAGGTGGCTGGTGGTCTTTTGCATCAGATTGGTTTGGTCCGGGATACTCCGTGCGCGCC

300 CTGCCATTCACTCTGAGCAATTACAGAAGATCCTATGAGGCCCTTCTCTCTCAGTGGCAGGTGGACATTCCCACCTGGGGAACATAACATCCTTTGGGGA

400 TGCTTTGGCACCATAAGGTGTCAACCCCTGATTGATGAAATGGTGTGGCTCGAATGTACCGCATCATGGAAAAGCAGGACAGGCTGCCTGGAAACAGGT

500 AGTGAGCGAGGCTACGCTGTCTCGCATTAGTAGTTTGGATGTGGTGGCTCATTTTTCAGGCATCTTGGCGCCATTGAAGCCGAGACCTGTAAATATCTGGCC

600 TCTCGGCTGCCCATGCTACACCACCTGGCGATGACAGGGTCAAAATGAACCATAGTGTATAATAGTACTTTGAATCAGGTGTTTGGTGTTCCTCCCAACCC

+ Start DRF3

700 CTGGTTCCCGGCCAAAGCTTCATGATTTCCAGCAATGGCTAAATAGCTGTACATTCCTCTCTATATTTTCTCTGTTCAGCTTCTTTGTACTCTTTTGTGTGT

*** Stop DRF2

800 GCTGTGGTTGCGGGTTCCAAATGCTACGTACTGTTTGGTTTCCGCTGGTTAGGGGCAATTTTCTTCGAACCTACGGTGAAATTACACGGTGTGCCGC

900 CTTGCCTCACCCGGCAAGCAGCCGCAGAGGCCCTACGAACCCGGCAGGTCCCTTTGGTGCAGGATAGGGCATGATCGATGTGGGAGGACGATCATGATGA

1000 ACTAGGGTTTGTGGTGCCGCTGCGCCTCTCCAGCGAAGGCCACTTGACCAGTGTCTACGCCCTGGTTGGCGTCCCTGTCCCTTCAGCTATACGGCCCAAGTTC

1100 CATCCCGAGATATTCGGGATAGGGAAATGTGAGTCGAGTCTATGTTGACATCAAGCACCATTCAATTTGGCTGTTTCATGATGGGAGAACACCACCTTGC

FIG. 20A

+ Start DRF4

CCCACCATGACAACATTTAGCCGTGCTTCAGACCTATTACCAGCATCAGGTCGACGGGGGCAATTGGTTTCACCTAGAATGGTGGGTCCTCCCTTCTTTC 1200

CTCTTGGTTGGTTTTAAATGTCCTCTGGTTTCTCAGGGCTTCGCCTGCAAGCCATGTTTCAGTTCGAGTCTTTTCAGACATCAAGACCAACACCACCGCAG 1300

*** Stop DRF3

CGGCAGGCTTTGCTGTCTCCCAAGACATCAGTTGCCTTAGGCATCGCAACTCGGCCTCTGAGCGGATTTCGCAAAAGTCCCTCAGTGGCGCACGGCGATAGG 1400

GACACCCGTGTATATCACTGTCACAGCCAATGTTACCGATGAGAAATTATTTGCATTCCCTCTGTATCTTCATGCTTTTCTTGGCTTTTCTATGCTTCT 1500

GAGATGAGTGAAAAGGGATTTAAGGTGGTATTTGGCAATGTGTAGGCATCGTGGCAGTGTGGCTCAACTTCACCAGTTACGTCCAACATGTCAAGGAAT 1600

TTACCCAACGTTCCCTTGGTAGTTGACCATGTGGGGCTGCTCCATTTCATGACGCCCCGAGACCATGAGGTGGGCAACGTTTTAGCCTGCTCTTTTACCAT 1700

*** Stop DRF4 + Start DRF5

TCGTGGCAATTTGAATGTTTAAGTAAGTGGGGGAAATGCTTGACCGGGGGCIGTTGCTCGCAATTGCTTTTTTATGGTGATCGTGCCGTCTGTT 1799

FIG. 20B

Consensus	TSSYSATGCTAMAMMAYCTGYGCAYGWAGGGTCAAAATGTRASCMTASWGTAYAAAYASYACKTTGRAYCRSGTGTKWGTCTRTYTTCCCMACSCCWGGTW	600
VR2385 DRF2	.GCCC.....C.CC.C...C...T.AC.....A.C.A..GT...T..T.GT...T...A.T.AG...TT...-G.T.....A..C..T...T	595
LV DRF2	.CGTG.....A.AA.T...-T...-C.TT--...-.....G.G.C..CA...C..C.CC...G...G.C.GC..-GA.....A.C.....C..G..A...A	580
Consensus	CSMGGCCMAAGYTKMMYGATTTCMRRCATGGCTMATMRSTGRCAYKCYTCYATWTTTCCCTCTGKGCWKCTCKKTACYYTKTYYRTWGTGCTKIG	700
VR2385 DRF2	.CC....A...C.TCAT.....CAG.....A..AGC...A..TT.C..T..A.....T...AG.T...TG...TC..TG.T.....G..	695
LV DRF2	.GA....C...T.GACC.....AGA.....C..CAG...G..CG.T..C..T.....G..TT.A...GT...CT.G..CA.A.....T..	680
Consensus	GYTKCGRRTTCCARYKCTACGYWMTGTTTTTGGTTCCRYTGGYMRSGGCAAYWYWCWTTTCGARCTSACGGTGA	776
VR2385 DRF2	.T.G..GG....ATG....TAC.....GC...TTAGG....TTTT..T.....A..C.....	771
LV DRF2	.C.T..AA....GCT.....CTA.....AT...CCCAC.....CACA..A.....G..G..-----	750

FIG. 21A. 1

Consensus	ATGGCTMATMRSTGTRCAYKCYTCYATWTTTTCCTCTGTGCKGWCWCTCKTKTACYYTKTTYRTWGTGCTKGGYTKCGRRTTCCARYKCTACGYWMIGTT	100
LV DRF3C..CAG...G..CG.T..C..T.....G..TT.A...GT...CT..G..CA.A....T...C.T..AA.....GCT.....CTA....	100
VR2385 DRF3A..AGC...A..TT.C..T..A.....T..AG.T...TG...TC.T..TG.T.....G...T.G..GG.....ATG.....TAC....	100
Consensus	TTTGGTTTCCRYTGGYMRSGGCAAYWWTCTTCGARCTSACRSRTSAAYTACACSRTRTGCMYGCCYTGYYACCMGKCAAGCRGCTCGCMRARGSCT	200
LV DRF3AT...CCCAC.....CACAA..A....G..G..CA.C..C....CA.A...AT...C..TTCI...A.T.....G.....CA.A.G..	200
VR2385 DRF3GC...TTAGG.....TTTT..T.....A..C..GG.G..T.....GG.G...CC...T..CCTC...C.G....A..-....AG.G.C..	199
Consensus	ACGARCCCGGYMGKWMCMTKTGGTGCARRATAGGGCATGAYMGRGTGTGRGGAGSRYGAYCATGATGARYTAGKKWWTGTCRSRTSCCGTCYGGSYWCKMCA	300
LV DRF3	-...G.....TC.TAA.A.G.....AA.....CA.G....A....CGT...C.....GT..-..TTAA...CA.C....C..GTA.GA..	298
VR2385 DRF3A.....CA.GTC.C.T.....GG.....TC.A....G....GAC..T.....AC...GGTT...-GG.G....T..CCT.TC..	298
Consensus	sRCGAMKSMMACTTGACSRGTMATTAYGCTGGYTGCGKTYYYTGTCCTTYWSCTAYRCGGCCARTTCCATCCSGAGWTRTTCGGGATAGGAATGTGWS	400
LV DRF3	A.--CTCAA.....-GG..TA...T..T...C...T.TTT.....TTC...CG.....A.....G...T.G.....TC	395
VR2385 DRF3	G...AGGCC.....CA..GC...C..C...T....G.CCC.....CAG...TA.....G.....C...A.A.....AG	398
Consensus	KCGMGCTWYGTGACAWSMRRCACCARTTCATTTTGYGCGVWKCATGATGGRCASAAWCMACCKTRYCYMMSRWSACAACATYTCMGKTRYWTSMG	500
LV DRF3	G..C....TC..G....AGCGA.....G.....T..C.AG.....T..C.AG.....A..C..TT.A...G.AT.TAC.GGAC.....C..C..AT.ATA.GC.	495
VR2385 DRF3	T..A....AT..T....TCAAG.....A.....C..T.TT.....G..G..CA.C...T.GC.CCA.CATG.....T..A..CG.GCT.CA.	498

FIG. 21B

Consensus	RCMTATTACCASCAYCARRTMGACGGGGGCAATTGGTTYCAYYTRGAATGGSTGGCKCCMYTCTTTTCYTCYTGGTGTYTMAAYRTMTCWTGGTTTC	600
LV DRF3	G. A. C. . C. . AA. A. C. . TT. G. C. G. . AC. T. . C. C. GC. C. . CA. A. . A.	595
VR2385 DRF3	A. C. G. . T. . GG. C. T. . CC. A. G. T. . CT. C. . T. T. . A. . TG. C. . T.	598
Consensus	TSAGGGGTTCCGCTGYAAGCCMTGTTTCWSKWCGRCTCTWTCAGAYATYRAGACCACACACACCGCRGCKGCMGGYTTYRYKGTCTCTYCARGACATCART	700
LV DRF3	. G. T. C. TCGA. . CA. . A. T. . TG. G. G. . T. . C. . T. . CATG. T. . G. A. .	695
VR2385 DRF3	. C. C. A. AGTT. . AG. . T. C. . CA. C. A. . G. . A. . C. . TGCT. C. . A. G. .	698
Consensus	TGYTYMGRCMTCACGGSRWCTCRGCAGCKCAWGAGRMRAATTCCTTCGSAAGTCGYCYCARTGYCGYGAMGCGWYRGTACTCCCCAGTACATCACGA	800
LV DRF3	. . TT. CC. A. C. GGT. . . A. G. . A. AAA. G. T. C. . A. . T. . T. . A. C. . TCG.	795
VR2385 DRF3	. . CC. TA. G. A. . ---. CAA. . . G. . --. T. . -T. . . GCG. ----- . . . C. -C. T. . G. . C. . C- . C. G. . ATA. -----	765
Consensus	TAA	803
LV DRF3	. . .	798
VR2385 DRF3	---	765

FIG. 21B.1

Consensus	M. WG. C. . K. L. W. L. SL. P. CL. SPSQ. G. WSF. S. WFAPR. SVRALPFTL. NYRRSYE. . L. . C. . D. P. KH	100
LV DRF2.	. Q. . H. GV. SASCSWTPS. SSLLV. LI-----PF. . ---. Y. . G. D. Y. . . . F. E. F. P. GL. PN. RP. V. QFAV. . .	90
VR2385 DRF2.	. K. . L. . --. ----AFLTK. AN-FL. MLSSSWCP. LI. . YFW. F. . A. V. W. . . A. D. Y. S. AF. SQ. QV. I. TWGT. . .	93
Consensus	PLGM. WH. . VS. LIDEMVSRR. Y. . ME. . GGAANKQVV. EATL. S. LD. V. HFQHLAA. EA. . C. . L. SRL. ML. . L. NV. YN. TL. . V. . . .	200
LV DRF2. F. . MR. . H. I. QT. . HS. G. TKL. G. . I. T. V. DS. RF. S. . . . V. . KN. AV--G. . SLQ. . I. . DR. ELI	188
VR2385 DRF2. L. . HK. . T. M. RI. . KA. S. SRI. S. . V. A. I. . ET. KY. A. . . P. . HH. RMTGS. . TIV. . S. . NQ. FAV	193
Consensus	FPTPG. RPKL. DF. QWLI. VH. SIFSSVA. S. TLF. VLWLR. P. LR. VFGF. W. . A.	264
LV DRF2. T. . . . T. . R. . . . S. . A. S. V. . . I. I. A. Y. . . . H. PT. ---THSS	249
VR2385 DRF2. S. . . . H. . Q. . . . A. . S. A. C. . . V. V. M. . T. . . . R. LG. IFLNSNR-	257

FIG. 22A

Consensus	MA, C,	FLC,	Y,	A,	S,	T, CFWFPL,	GN, SFELT, NYT, C, PC, T, QAA,	EPGR,	WC, IGHDRC, E, DHDEL,	PSG,	100
LV DRF3,	HQ, ARFHF,	GFIC, LVHS, LASN, SS, L,	AH, T,	I,	I, M, S, S,	RQRL,	NM, K,	E, R,	LMSI,	YDN 100
VR2385 DRF3,	NS, TFLYI,	CSFL, SFCC, VVAG, NA, Y,	VR, F,	V,	V, P, L, R,	AEAY,	SL, R,	G, D,	GFVV,	LSS 100
Consensus	L,	YAWLA, LSFSY, AQFHPE, FGIGNVSRV, VD,	HQFICA, HDG, N, T,	NISA,	YY, HQ, DGGNWFHLEW, RP, FSSWLVLN, SWFL	200				
LV DRF3,	L-K, EGY,	F,	A,	L,	F, KR,	E, H, S, VSTGH,	LYAA, H, I,	L, L,	I,	199
VR2385 DRF3,	EGH, TSA,	S,	T,	I,	Y, IK,	V, Q, T, LPHHD,	VLQT, Q, V,	V, F,	V,	200
Consensus	RRSP, S, VS, R, Q, RPT, P,	S,	TS,	L,	R, F,	K, S,				266
LV DRF3,	V, P, R, IY, IL,	R, RLPVSW, FR,	IVSD, TGSQQRK, K, PSESPPNVV, P, VLPSTSR						265
VR2385 DRF3,	A, H, V, VF, TS,	P, QRQALL, SK, V--A, GIATRPL, R, A-----, - , LSAARR-							255

FIG. 22B

Consensus	M, A,	LF, L, G,	VS, AFACKPCFS,	LSDI, TINTAAAGF, VLQDI, C, R,	A, E, I,	K, QCR, A, GTP, YIT, TANVTDE, YL,	DL 100				
LV DRF4,	A, AT,	F, A, AQHIM, E,	TH,	E,	M,	N, F, PHGVSA, Q, K, SFG, SS,	E, V,	Q, I,	S, YNA,	100
VR2385 DRF4,	G, SL,	L, V, FKCLL, Q,	SS,	K,	A,	S, L, HR--NS, S, A, R--, VP,	T, I,	V,	N, HSS,	96
Consensus	LMLS, CLFYASEMSEKGFV, FGNVSG, V,	CVNFT, YV, HV,	TQ,	V,	RLHF, TP, MRWAT,	ACLF, ILLAI,				184
LV DRF4,	A,	I,	V, SA,	D, A, TQH, QHHL, IDHI,	L, SA,	TI,	A,	183
VR2385 DRF4,	S,	V,	I, AV,	S, Q, KEF, RSLV, DH-V,	M, ET,	VL,	T,	179

FIG. 22C

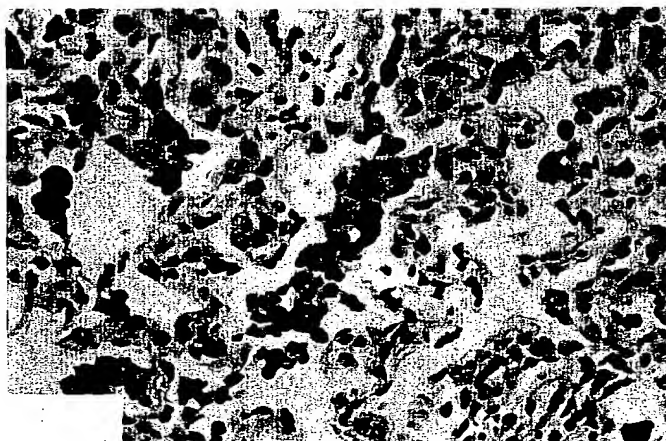


FIG.23

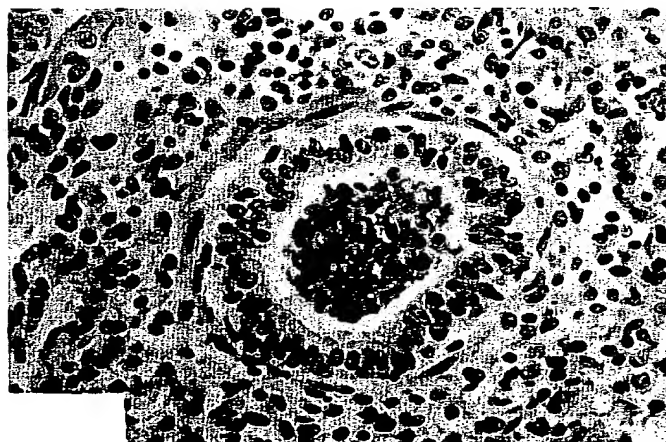


FIG.24

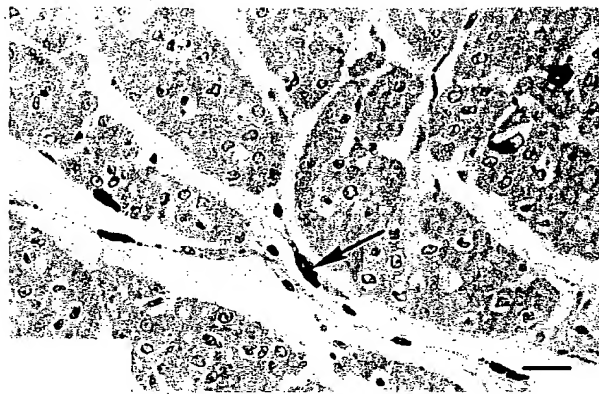


FIG.25

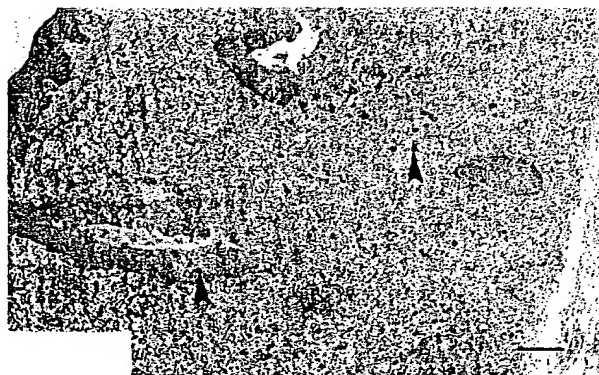


FIG.26

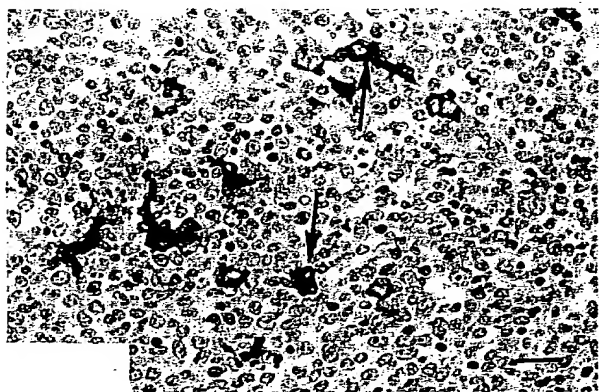


FIG.27



FIG. 28A

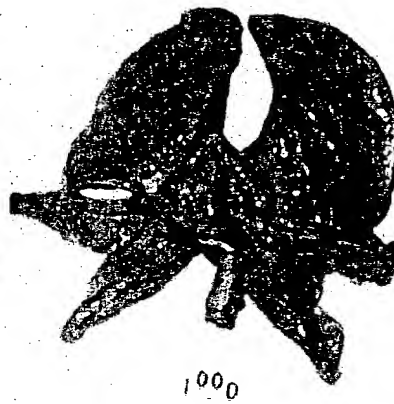


FIG. 28B



FIG. 28C

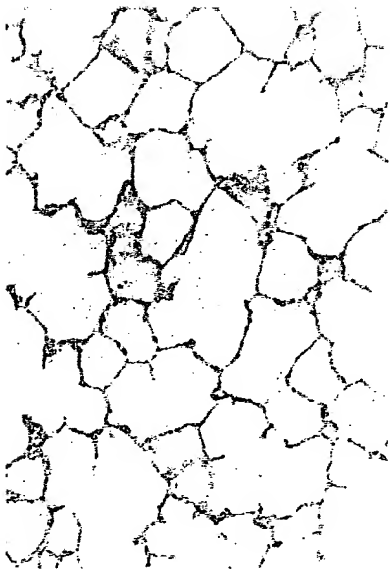


FIG. 29A



FIG. 29B

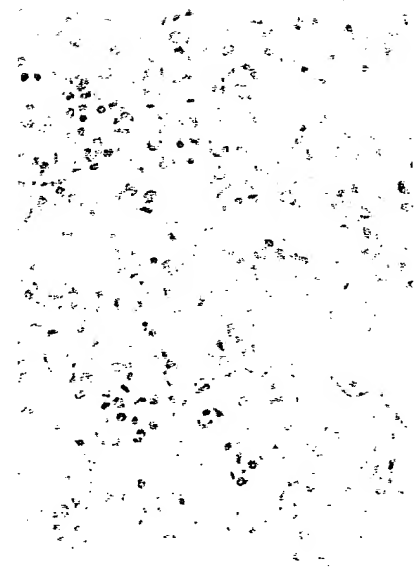
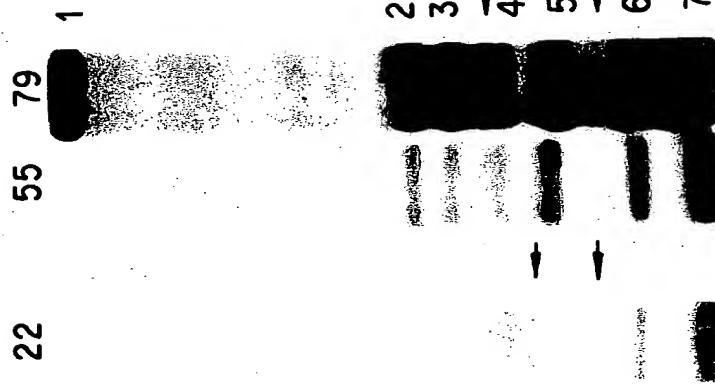


FIG. 29C

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1

2 3 4 5 6 7

FIG.30A

FIG.30B

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